

ABSTRACT

The invention is directed to a method of diagnosing a cell proliferative disorder of breast tissue by determining the methylation status of nucleic acids obtained from a subject. Aberrant methylation of several genes including TWIST, HOXA5, NES-1, retinoic acid receptor beta (RAR β), estrogen receptor (ER), cyclin D2, WT-1, 14.3.3 sigma, HIN-1, RASSF1A, and combinations of such genes serve as markers of breast malignancy.